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============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2011; month=5; day=4; hr=15; min=49; sec=41; ms=312; ]
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Application No: 10577893   Version No: 2.0

Input Set:

Output Set:

            Started: 2011-04-27 17:46:59.122
           Finished: 2011-04-27 17:47:01.361
            Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 239 ms
     Total Warnings: 28
       Total Errors: 0
No. of SeqIDs Defined: 28
  Actual SeqID Count: 28

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (1)

W   213   Artificial or Unknown found in <213> in SEQ ID (2)

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

W   213   Artificial or Unknown found in <213> in SEQ ID (6)

W   213   Artificial or Unknown found in <213> in SEQ ID (7)

W   213   Artificial or Unknown found in <213> in SEQ ID (8)

W   213   Artificial or Unknown found in <213> in SEQ ID (9)

W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (15)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (17)

W   213   Artificial or Unknown found in <213> in SEQ ID (18)

W   213   Artificial or Unknown found in <213> in SEQ ID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-04-27 17:46:59.122

Finished: 2011-04-27 17:47:01.361

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 239 ms

Total Warnings: 28

Total Errors: 0

No. of SeqIDs Defined: 28

Actual SeqID Count: 28

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<110> Ludmerer, Steven W.

      Graham, Donald J.

      LaFemina, Robert L.

      Flores, Osvaldo A.

      Pizzuti, Maura

      Traboni, Cinzia

<120> HCV REPLICONS CONTAINING NS5B FROM
  GENOTYPE 2B

<130> 21564YP

<140> 10577893
<141> 2011-04-27

<150> PCT/US2004/036575
<151> 2004-11-03

<150> 60/517,605
<151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> HCV

<221> VARIANT
<222> (5)...(5)
<223> Xaa = threonine or serine

<221> VARIANT
<222> (24)...(24)
<223> Xaa = asparagine or serine

<221> VARIANT
<222> (31)...(31)
<223> Xaa = methionine or isoleucine

<221> VARIANT
<222> (392)...(392)
<223> Xaa = isoleucine or leucine

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Ser Met Ser Tyr Xaa Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro
1   5   10   15
Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg

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                20                      25                      30
Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg
          35                      40                      45
Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr
    50                      55                      60
Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala
65                      70                      75                      80
Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser
                85                      90                      95
Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser
                100                     105                     110
Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu
          115                     120                     125
Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
    130                     135                     140
Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu Ile
145                     150                     155                     160
Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
                165                     170                     175
Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly
                180                     185                     190
Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp
          195                     200                     205
Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
          210                     215                     220
Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr
225                     230                     235                     240
Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu
                245                     250                     255
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln
                260                     265                     270
Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser
          275                     280                     285
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys
    290                     295                     300
Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu
305                     310                     315                     320
Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu
                325                     330                     335
Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
          340                     345                     350
Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
          355                     360                     365
Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe Leu
    370                     375                     380
Thr Arg Asp Pro Thr Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val
385                     390                     395                     400
Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala
                405                     410                     415
Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile
                420                     425                     430
Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr
          435                     440                     445
Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu
    450                     455                     460
Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His
465                     470                     475                     480
```

```
Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro
                485             490                 495
Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile
            500             505             510
Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp
        515             520             525
Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg
    530             535             540
Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp Ile
545             550             555                 560
Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Leu Cys Leu
            565             570             575
Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg
            580             585                 590
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<210> 2
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> HCV

<221> variation
<222> (3)...(3)
<223> n = A or T

<221> variation
<222> (9)...(9)
<223> n = C or A

<221> variation
<222> (13)...(13)
<223> n = A or T

<221> variation
<222> (15)...(15)
<223> n = A or C

<221> variation
<222> (21)...(21)
<223> n – A or G

<221> variation
<222> (24)...(24)
<223> n = C or G

<221> variation
<222> (28)...(28)
<223> n = T or C

<221> modified_base
<222> (30)...(30)
<223> n = G or C

<221> variation

<222> (33)...(33)
<223> n = C or A

<221> variation
<222> (71)...(71)
<223> n = A or G

<221> variation
<222> (93)...(93)
<223> n = G or T

<221> variation
<222> (1174)...(1174)
<223> n = A or C

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ttaccgatca nccctctgag taattcgctc atncggttcc ataataaggt gtactccaca   120
acctcgagga gtgcctctct gagggcaaag aaggtgactt ttgacagggt gcaggtgctg   180
gacgcacact atgactcagt cttgcaggac gttaagcggg ccgcctctaa ggttagtgcg   240
aggctcctca cggtagagga agcctgcgcg ctgacccgc cccactccgc caaatcgcga   300
tacggatttg gggcaaaaga ggtgcgcagc ttatctagga gggccgttaa ccacatccgg   360
tccgtgtggg aggacctcct ggaagaccaa catacccaa ttgacacaac tatcatggct   420
aaaaatgagg tgttctgcat tgatccaact aaaggtggga aaaagccagc tcgcctcatc   480
gtataccccg accttggggt cagggtgtgc gaaaagatgg ccctctatga catcgcacaa   540
aagcttccca aagcgataat ggggccatcc tatgggttcc aatactctcc cgcagaacgg   600
gtcgatttcc tcctcaaagc ttggggaagt aagaaggacc caatgggggtt ctcgtatgac   660
acccgctgct ttgactcaac cgtcacggag agggacataa gaacagaaga atccatatat   720
caggcttgtt ctctgcctca agaagccaga actgtcatac actcgctcac tgagagactt   780
tacgtaggag ggcccatgac aaacagcaaa gggcaatcct gcggctacag cgttgccgc   840
gcaagcggtg ttttcaccac cagcatgggg aataccatga catgttacat caaagccctt   900
gcagcgtgta aggctgcagg gatcgtggac cctgttatgt tggtgtgtgg agacgacctg   960
gtcgtcatct cagagagcca aggtaacgag gaggacgagc gaaacctgag agctttcacg 1020
gaggctatga ccaggtattc cgcccctccc ggtgaccttc ccagaccgga atatgacttg 1080
gagcttataa catcctgctc ctcaaacgta tcggtagcgc tggactctcg gggtcgccgc 1140
cggtacttcc taaccagaga ccctaccact ccantcaccc gagctgcttg ggaaacagta 1200
agacactccc ctgtcaattc ttggctgggc aacatcatcc agtacgcccc cacaatctgg 1260
gtccggatgg tcataatgac tcacttcttc tccatactat tggcccagga cactctgaac 1320
caaaatctca attttgagat gtacggggca gtatactcgg tcaatccatt agacctaccg 1380
gccataattg aaaggctaca tgggcttgaa gccttttcac tgcacacata ctctccccac 1440
gaactctcac gggtggcagc aactctcaga aaacttggag cgcctcccct tagagcgtgg 1500
aagagtcggg cgcgtgccgt gagagcttca ctcatcgccc aaggagcgag ggcggccatt 1560
tgtggccgct acctcttcaa ctgggcggtg aaaacaaagc tcaaactcac tccattgccc 1620
gaggcgagcc gcctggattt atccgggtgg ttcaccgtgg gcgccggcgg gggcgacatt 1680
tatcacagcg tgtcgcatgc ccgaccccgc ctattactcc tttgcctact cctacttagc 1740
gtaggagtag gcatctttttt actccccgat cgatga   1776

<210> 3
<211> 1394
<212> PRT
<213> Artificial Sequence

<220>
<223> HCV

<221> VARIANT
<222> (1215)...(1215)

<223> Xaa = asparagine or serine

<221> VARIANT
<222> (904)...(904)
<223> Xaa = valine or alanine

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1   5   10   15
Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
            20   25   30
Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
        35   40   45
Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
    50   55   60
Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
65   70   75   80
Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr
                85   90   95
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
            100   105   110
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
            115   120   125
Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
    130   135   140
Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
145   150   155   160
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
                165   170   175
Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
                180   185   190
Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
        195   200   205
Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
    210   215   220
Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
225   230   235   240
Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
                245   250   255
Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly
                260   265   270
Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
        275   280   285
Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
        290   295   300
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
305   310   315   320
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
                325   330   335
Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
                340   345   350
Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe
            355   360   365
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
    370   375   380
Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
385   390   395   400

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Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met
            405               410               415
Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
            420               425               430
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
            435               440               445
Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly
      450               455               460
Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly
465               470               475               480
Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
                  485               490               495
Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val
                  500               505               510
Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
            515               520               525
His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
      530               535               540
Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
545               550               555               560
Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
                  565               570               575
Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
            580               585               590
Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
      595               600               605
Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met
      610               615               620
Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
625               630               635               640
Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val
                  645               650               655
Ile Val Gly Arg Ile Ile Leu Ser Gly Arg Pro Ala Ile Val Pro Asp
                  660               665               670
Arg Glu Phe Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ala Ser
            675               680               685
His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys
      690               695               700
Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala
705               710               715               720
Ala Ala Pro Val Val Glu Ser Lys Trp Arg Ala Leu Glu Thr Phe Trp
                  725               730               735
Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly
                  740               745               750
Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
            755               760               765
Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Ser Thr Leu Leu Phe
      770               775               780
Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
785               790               795               800
Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val Gly Ser
                  805               810               815
Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
                  820               825               830
Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Met
            835               840               845
Pro Ser Thr Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
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Gly Ala Leu Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His
865   870   875   880
Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
                    885   890   895
Phe Ala Ser Arg Gly Asn His Xaa Ser Pro Thr His Tyr Val Pro Glu
                900   905   910
Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
            915   920   925
Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
        930   935   940
Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys
945   950   955   960
Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro
                965   970   975
Gln Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly
                980   985   990
Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala
            995   1000   1005
Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro
        1010   1015   1020
Lys Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr
1025   1030   1035   1040
Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala
                1045   1050   1055
Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly
            1060   1065   1070
Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro
        1075   1080   1085
Cys Gln Val Pro Ala